RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
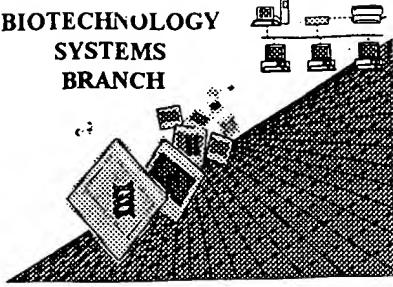BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/894,912_

Source: _OIPE_

Date Processed by STIC: _7/18/2001_

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2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
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Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
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RAW SEQUENCE LISTING   DATE: 07/18/2001
PATENT APPLICATION: US/09/894,912   TIME: 10:30:01

Input Set : A:\37260Aseq.txt
Output Set: N:\CRF3\07182001\I894912.raw


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  5 <110> APPLICANT: Tang et al.
  8 <120> TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH
FACTOR-LIKE
  9       POLYPEPTIDES AND POLYNUCLEOTIDES
 12 <130> FILE REFERENCE: 28110/37260A
 14 <140> CURRENT APPLICATION NUMBER: US/09/894,912
 15 <141> CURRENT FILING DATE: 2001-06-28
 17 <150> PRIOR APPLICATION NUMBER: To be assigned
 18 <151> PRIOR FILING DATE: 2001-04-05
 20 <150> PRIOR APPLICATION NUMBER: 60/266,614
 21 <151> PRIOR FILING DATE: 2001-02-05
 23 <150> PRIOR APPLICATION NUMBER: 60/215,733
 24 <151> PRIOR FILING DATE: 2000-06-28
 26 <150> PRIOR APPLICATION NUMBER: 09/757,562
 27 <151> PRIOR FILING DATE: 2001-01-09
 29 <150> PRIOR APPLICATION NUMBER: 09/543,774
 30 <151> PRIOR FILING DATE: 2000-04-05
 33 <160> NUMBER OF SEQ ID NOS: 48
 35 <170> SOFTWARE: PatentIn version 3.0
 39 <210> SEQ ID NO: 1
 40 <211> LENGTH: 301
 41 <212> TYPE: DNA
 42 <213> ORGANISM: Homo sapiens
 44 <400> SEQUENCE: 1
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 47 gtaaagaagc aatacctgac agcaaaagtc tggaatccag caaagaaatc ccagagcaac      120
 49 gagaaaacaa acagcagcag aagaagcgaa aagtccaaga taaacagaaa tcggtatcag      180
 51 tcagcactgt acactagagg gttccatgag attattgtag actcatgatg ctgctatctc      240
 53 aaccagatgc ccaggacagg tgctctagcc attaggacca caaatggaca tgtcagttat      300
 55 t                                                                      301
 58 <210> SEQ ID NO: 2
 59 <211> LENGTH: 392
 60 <212> TYPE: DNA
 61 <213> ORGANISM: Homo sapiens
 63 <400> SEQUENCE: 2
 64 tggaactcga tatccagata taaataagcg tacaaaatgc aaagctgact gtgatacctg       60
 66 tttcaacaaa gatttctgca caaaatgtaa aagtggattt tacttacacc ttggaaagtg      120
 68 ccttgacaat tgcccagaag ggttggaagc caacaaccat actatggagt gtgtcagtat      180
 70 tgtgcactgt gaggtcagtg aatggaatcc ttggagtcca tgcacgaaga agggaaaaac      240
 72 atgtggcttc aaaagaggga ctgaaacacg ggtccgagaa ataatacagc atccttcagc      300
 74 aaagggtaac ctatgtcccc caacaaatga gacaagaaag tgtacagtgc aaaggaagaa      360
 76 gtgtcagaag ggagaacgag gaaaataagg ag                                    392
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 80 <211> LENGTH: 475
 81 <212> TYPE: DNA
 82 <213> ORGANISM: Homo sapiens
 84 <220> FEATURE:
 85 <221> NAME/KEY: misc_feature
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Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING   DATE: 07/18/2001
PATENT APPLICATION: US/09/894,912   TIME: 10:30:01

Input Set : A:\37260Aseq.txt
Output Set: N:\CRF3\07182001\I894912.raw

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      91 <400> SEQUENCE: 3
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W-->  94 ccacgcgtnc gcccacgcgt ccggagagga aaagaaaaaa acctaattta ggagaaagta   120
      96 aagaagcaat acctgacagc ggaagtctgg aatggagcaa agaaatccca gagcaacgag   180
      98 aaaacaaaca gcagcagaag aagcgaaaag tccaagataa acagaaatcg gtatcagtca   240
     100 gcactgtaca ctagagggtt ccatgagatt attgtagact catgatgctg ctatctcaac   300
     102 cagatgccca ggacaggtgc tctagccatt aggaccacaa atggacatgt cagttattgc   360
     104 tctgtctaaa caacattccc agtagttgct atattcttca tacaagcata gttaacaaca   420
W--> 106 aagagccaaa agatcaaaga agggatactt tcagatggtt gtcttgtgtg cttcn        475
     109 <210> SEQ ID NO: 4
     110 <211> LENGTH: 473
     111 <212> TYPE: DNA
     112 <213> ORGANISM: Homo sapiens
     114 <220> FEATURE:
     115 <221> NAME/KEY: misc_feature
     117 <222> LOCATION: (1)..(473)
     118 <223> OTHER INFORMATION: n = A, T, G, or C
     121 <400> SEQUENCE: 4
     122 tgggcannnn aaanttttga nattcgatcc gcgctgcagg aattcggcac gagacgagga    60
     124 aaaaaaggaa gggagaggaa aagaaaaaaa cctaataaag gagaaagtaa agaagcaata   120
     126 cctgacagca aaagtctgga atccagcaga gaaatcccag agcaacgaga aaacaaacag   180
     128 cagcagaaga agcgaaaagt ccaagataaa cagaaatcgg tatcagtcag cactgtacac   240
     130 tagagggttc catgagatta ttgtagactc atgatgctgc tatctcaacc agatgcccag   300
     132 gacaggtgct ctagccatta ggaccacaaa tggacatgtc agttattgct ctgtctaaac   360
     134 aacattccca gtagttgcta tattcttcat acaagcatag ttaacaacaa agagccaaaa   420
     136 gatcaaagaa gggatacttt cagatggttg tcttgtgtgc ttctctgcat ttt           473
     139 <210> SEQ ID NO: 5
     140 <211> LENGTH: 462
     141 <212> TYPE: DNA
     142 <213> ORGANISM: Homo sapiens
     145 <220> FEATURE:
     146 <221> NAME/KEY: misc_feature
     148 <222> LOCATION: (1)..(462)
     149 <223> OTHER INFORMATION: n = A, T, G, or C
     152 <400> SEQUENCE: 5
     153 tgggagannn ntttgaaact gagatcgtcg canacncnac nangaataaa aggaagggag    60
     155 aaggaaagaa aaaaacctaa taaaggagaa agtaaagaat caatttctga cagcaaaagt   120
     157 ctggaatcca tcaaagaaat cccatatcaa cgagaaaaca gacagcagca caaaaagcga   180
     159 aaagtccaag ataaacagaa atcggtatca gtcagcactg tacactagag ggttccatga   240
     161 gattattgta gactcatgat gctgctatct caaccagatg cccaggacag gtgctctatc   300
     163 cattacgacc acaaatggac atgtcagtta ttgctctgtc taaacaacat tcccagtagt   360
     165 tgctatattc ttcatacaag catagttaac aacaaagagc caaaagatca agaagggat    420
     167 actttcagat ggttgtcttg tgtgcttctc tgcattttta aa                      462
     170 <210> SEQ ID NO: 6
     171 <211> LENGTH: 384
     172 <212> TYPE: DNA
     173 <213> ORGANISM: Homo sapiens
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RAW SEQUENCE LISTING   DATE: 07/18/2001
PATENT APPLICATION: US/09/894,912   TIME: 10:30:02

Input Set : A:\37260Aseq.txt
Output Set: N:\CRF3\07182001\I894912.raw

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176 <400> SEQUENCE: 6
177 aataatgtgt acaaaatgca aagctgactg tgatacctgt ttcaacaaaa atttctgcac      60
179 aaaatgtaaa agtggatttt acttacacct tggaaagtgc cttgacaatt gcccagaagg     120
181 gttggaagcc aacaaccata ctatggagtg tgtcagtatt gtgcactgtg aggtcagtga     180
183 atggaatcct tggagtccat gcacgaagaa gggaaaaaca tgtggcttca aaagagggac     240
185 tgaaacacgg gtccgagaaa taatacagca tccttcagca aagggtaacc tatgtccccc     300
187 aacaaatgag acaagaaagt gtacagtgca aaggaagaag tgtcagaagg gagaacgagg     360
189 aaaaaaagga agggagagga aaag                                             384
192 <210> SEQ ID NO: 7
193 <211> LENGTH: 390
194 <212> TYPE: DNA
195 <213> ORGANISM: Homo sapiens
197 <220> FEATURE:
198 <221> NAME/KEY: misc_feature
200 <222> LOCATION: (1)..(390)
201 <223> OTHER INFORMATION: n = A, T, G, or C
204 <400> SEQUENCE: 7
205 cgttgctctg ggatttcttt gctggattcc agacttttgc tgtcaggtat tgcttcttta      60
207 ctttctcctt tattaggttt ttttcttttc ctctcccttc cttttttttcc tcgttctccc    120
209 ttctgacact tcttcctttg cactgtacac tttcttgtct catttgttgg gggacatagg     180
211 ttaccctttg ctgaaggatg ctgtattatt tctcggaccc gtgtttcagt ccctcttttg     240
213 aagccacatg tttttccctt cttcgtgcat ggactccaag gattccattc actgacctca     300
215 cagtgcacaa tactgacaca ctccatagta tggttgttgg cttccaaccc ttctgggcaa     360
217 ttgtcaaggc actttccaag gtgtaagtan                                       390
220 <210> SEQ ID NO: 8
221 <211> LENGTH: 1345
222 <212> TYPE: DNA
223 <213> ORGANISM: Homo sapiens
225 <220> FEATURE:
226 <221> NAME/KEY: misc_feature
228 <222> LOCATION: (321)..(1235)
229 <223> OTHER INFORMATION: similar to gi4519541 in the genpept database release 114,
Run wit
230        h FASTXY3.3t00, default parameter
233 <400> SEQUENCE: 8
234 gcggccgccc cggcggctcc tggaaccccg gttcgcggcg atgccagcca ccccagcgaa      60
236 gccgccgcag ttcagtgctt ggataatttg aaagtacaat agttggtttc cctgtccacc     120
238 cgccccactt cgcttgccat cacagcacgc ctatcggatg tgagaggaga agtcccgctg     180
240 ctcgggcact gtctatatac gcctaacacc tacatatatt ttaaaaacat taaatataat     240
242 taacaatcaa aagaaagagg agaaaggaag ggaagcatta ctgggttact atgcacttgc     300
244 gactgatttc ttggcttttt atcattttga actttatgga atacatcggc agccaaaacg     360
246 cctcccgggg aaggcgccag cgaagaatgc atcctaacgt tagtcaaggc tgccaaggag     420
248 gctgtgcaac atgctcagat tacaatggat gtttgtcatg taagcccaga ctattttttg     480
250 ctctggaaag aattggcatg aagcagattg gagtatgtct catcttcatg tccaagtgga     540
252 tattatggaa ctcgatatcc agatataaat aatgtgtaca aaatgcaaag ctgactgtga     600
254 tacctgtttc aacaaaaatt tctgcacaaa atgtaaaagt ggattttact tacaccttgg     660
256 aaagtgcctt gacaattgcc cagaagggtt ggaagccaac aaccatacta tggagtgtgt     720
258 cagtattgtg cactgtgagg tcagtgaatg gaatccttgg agtccatgca cgaagaaggg     780
260 aaaaacatgt ggcttcaaaa gagggactga acacgggtc cgagaaataa tacagcatcc     840
262 ttcagcaaag ggtaacctat gtcccccaac aaatgagaca agaaagtgta cagtgcaaag     900
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264 gaagaagtgt cagaagggag aacgaggaaa aaaaggaagg gagaggaaaa gaaaaaaacc   960
266 taataaagga gaaagtaaag aagcaatacc tgacagcaaa agtctggaat ccagcaaaga  1020
268 aatcccagag caacgagaaa acaaacagca gcagaagaag cgaaaagtcc aagataaaca  1080
270 gaaatcggta tcagtcagca ctgtacacta gagggttcca tgagattatt gtagactcat  1140
272 gatgctgcta tctcaaccag atgcccagga caggtgctct agccattagg accacaaatg  1200
274 gacatgtcag ttattgctct gtctaaacaa cattcccagt agttgctata ttcttcatac  1260
276 aagcatagtt aacaacaaag agccaaaaga tcaaagaagg gatactttca gatggttgtc  1320
278 ttgtgtgctt ctctgcattt ttaaa                                        1345
281 <210> SEQ ID NO: 9
282 <211> LENGTH: 1343
283 <212> TYPE: DNA
284 <213> ORGANISM: Homo sapiens
286 <220> FEATURE:
287 <221> NAME/KEY: CDS
289 <222> LOCATION: (291)..(1109)
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293 gcggccgccc cggcggctcc tggaaccccg gttcgcggcg atgccagcca ccccagcgaa    60
295 gccgccgcag ttcagtgctt ggataatttg aaagtacaat agttggtttc cctgtccacc   120
297 cgccccactt cgcttgccat cacagcacgc ctatcggatg tgagaggaga agtcccgctg   180
299 ctcgggcact gtctatatac gcctaacacc tacatatatt ttaaaaacat taaatataat   240
301 taacaatcaa aagaagagg agaaaggaag ggaagcatta ctgggttact atg cac        296
302                                                        Met His
303                                                        1
305 ttg cga ctg att tct tgg ctt ttt atc att ttg aac ttt atg gaa tac     344
306 Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met Glu Tyr
307         5                   10                  15
309 atc ggc agc caa aac gcc tcc cgg gga agg cgc cag cga aga atg cat     392
310 Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg Met His
311     20                  25                  30
313 cct aac gtt agt caa ggc tgc caa gga ggc tgt gca aca tgc tca gat     440
314 Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys Ser Asp
315 35                  40                  45                  50
319 tac aat gga tgt ttg tca tgt aag ccc aga cta ttt ttt gct ctg gaa     488
320 Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala Leu Glu
321                 55                  60                  65
323 aga att ggc atg aag cag att gga gta tgt ctc tct tca tgt cca agt     536
324 Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys Pro Ser
325             70                  75                  80
327 gga tat tat gga act cga tat cca gat ata aat aag tgt aca aaa tgc     584
328 Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr Lys Cys
329         85                  90                  95
331 aaa gct gac tgt gat acc tgt ttc aac aaa aat ttc tgc aca aaa tgt     632
332 Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys
333     100                 105                 110
335 aaa agt gga ttt tac tta cac ctt gga aag tgc ctt gac aat tgc cca     680
336 Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn Cys Pro
337 115                 120                 125                 130
339 gaa ggg ttg gaa gcc aac aac cat act atg gag tgt gtc agt att gtg     728
340 Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser Ile Val
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341                    135                140                145
343 cac tgt gag gtc agt gaa tgg aat cct tgg agt cca tgc acg aag aag      776
344 His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys
345                    150                155                160
347 gga aaa aca tgt ggc ttc aaa aga ggg act gaa aca cgg gtc cga gaa      824
348 Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val Arg Glu
349           165                170                175
351 ata ata cag cat cct tca gca aag ggt aac cta tgt ccc cca aca aat      872
352 Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro Thr Asn
353       180                185                190
355 gag aca aga aag tgt aca gtg caa agg aag aag tgt cag aag gga gaa      920
356 Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys Gly Glu
357 195                200                205                210
359 cga gga aaa aaa gga agg gag agg aaa aga aaa aaa cct aat aaa gga      968
360 Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn Lys Gly
361                    215                220                225
363 gaa agt aaa gaa gca ata cct gac agc aaa agt ctg gaa tcc agc aaa     1016
364 Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser Ser Lys
365                    230                235                240
367 gaa atc cca gag caa cga gaa aac aaa cag cag cag aag aag cga aaa     1064
368 Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys Arg Lys
369           245                250                255
371 gtc caa gat aaa cag aaa tcg gta tca gtc agc act gta cac tag        1109
372 Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His
373       260                265                270
375 agggttccat gagattattg tagactcatg atgctgctat ctcaaccaga tgcccaggac   1169
377 aggtgctcta gccattagga ccacaaatgg acatgtcagt tattgctctg tctaaacaac   1229
379 attcccagta gttgctatat tcttcataca agcatagtta acaacaaaga gccaaaagat   1289
381 caaagaaggg atactttcag atggttgtct tgtgtgcttc tctgcatttt taaa         1343
384 <210> SEQ ID NO: 10
385 <211> LENGTH: 272
386 <212> TYPE: PRT
387 <213> ORGANISM: Homo sapiens
390 <400> SEQUENCE: 10
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393 1                 5                 10                15
396 Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
397               20                25                30
400 Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
401           35                40                45
404 Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
405       50                55                60
408 Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
409 65                70                75                80
412 Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
413               85                90                95
416 Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
417           100                105                110
420 Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn
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<210> 31
<211> 2384
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (511)..(1347)

<400> 31

see next page for *erased* portion of seq. 31

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tctaacaagg tgtatctagt aggagagaaa gccaccacaa taaatatatt tgttaatag(n)2367

taaaaaaaaa aaaaaaa                                                2384
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see item 9 on Error summary sheet

→ **Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.**

Input Set : **A:\37260Aseq.txt**
Output Set: **N:\CRF3\07182001\I894912.raw**

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L:14 M:270 C: Current Application Number differs, Replaced Application Number
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1201 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:31
L:1201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
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